



IFWO

RAW SEQUENCE LISTING

DATE: 07/22/2004

PATENT APPLICATION: US/10/820,202

TIME: 10:10:18

Input Set : A:\Carnegie 56100 5005 US 01.txt

Output Set: N:\CRF4\07222004\J820202.raw

3 <110> APPLICANT: Broun, Pierre
 4 Boddupalli, Sekhar S
 5 Somerville, Chris S
 6 Van de Loo, Frank
 8 <120> TITLE OF INVENTION: PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY
 MODIFIED

9 PLANTS
 11 <130> FILE REFERENCE: 56100-5005-01-US
 13 <140> CURRENT APPLICATION NUMBER: US 10/820,202
 14 <141> CURRENT FILING DATE: 2004-04-08
 16 <150> PRIOR APPLICATION NUMBER: US 09/117,921
 17 <151> PRIOR FILING DATE: 1999-03-04
 19 <160> NUMBER OF SEQ ID NOS: 15
 21 <170> SOFTWARE: PatentIn version 3.2
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 543
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Artificial sequence
 28 <220> FEATURE:
 29 <223> OTHER INFORMATION: Nucleotide sequence of pLesq2
 32 <220> FEATURE:
 33 <221> NAME/KEY: misc_feature
 34 <222> LOCATION: (83)..(83)
 35 <223> OTHER INFORMATION: n is a, c, g, or t
 37 <400> SEQUENCE: 1



38 tattggcacc ggcggcacca ttccaacaat ggatccctag aaaaagatga agtctttgtc 60
 W--> 40 ccacctaaaga.aagctgcagt canatgggtat gtcaaataacc tcaacaaccc tcttggacgc 120
 42 attctggtgt taacagttca gtttatectc ggggtggcctt tgtatctagc ctttaatgta 180
 44 tcaggtagac cttatgatgg ttctgcttca catttcttcc ctcatgcacc tatctttaag 240
 46 gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctgttatggt 300
 48 ctttaccggt acgctgcttc acaaggattg actgctatga tctgcgtcta cggagtaccg 360
 50 cttttgatag tgaacttttt ccttgtcttg gtcactttct tgcagcacac tcatecttca 420
 52 ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggt tacggtagac 480
 54 agagactatg gaatcttgaa caaggtgttt cacaacataa cagacaccca cgtagcacac 540
 56 cac 543
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 544
 61 <212> TYPE: DNA
 62 <213> ORGANISM: Artificial sequence
 64 <220> FEATURE:
 65 <223> OTHER INFORMATION: Nucleotide sequence of pLesq3
 67 <400> SEQUENCE: 2
 68 tataggcacc ggaggcacca ttccaacaca ggatccctcg aaagagatga agtatattgtc 60
 70 ccaaagcaga aatccgcaat caagtgttac ggccaatacc tcaacaaccc tcttggctgc 120

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72 atcatgatgt taactgtcca gtctgtcttc ggatggccct tgtacttagc cttcaacgtt      180
74 tctggcagac cctacaatgg ttctgcttcc catttcttcc ccaatgctcc tatctacaac      240
76 gaccgtgaac gcctccagat ttacatctct gatgctggta ttctagccgt ctgttatggg      300
78 ctttaccggt acgctgttgc acaaggacta gcctcaatga tctgtctaaa cggagttccg      360
80 cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcacctgcg      420
82 ttgcctcact atgattcacc agagtgggat tggttagag gagctttagc tactgtagac      480
84 agagactatg gaatcttgaa caagggtgtc cataacatca cagacaccca cgctgcacac      540
86 cact                                                                    544
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90 <211> LENGTH: 1855
91 <212> TYPE: DNA
92 <213> ORGANISM: Artificial sequence
94 <220> FEATURE:
95 <223> OTHER INFORMATION: Nucleotide sequence of genomic clone encoding pLesq-HYD
98 <220> FEATURE:
99 <221> NAME/KEY: misc_feature
100 <222> LOCATION: (46)..(46)
101 <223> OTHER INFORMATION: n is a, c, g, or t
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104 <221> NAME/KEY: misc_feature
105 <222> LOCATION: (99)..(99)
106 <223> OTHER INFORMATION: n is a, c, g, or t
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119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: (1788)..(1788)
121 <223> OTHER INFORMATION: n is a, c, g, or t
123 <400> SEQUENCE: 3
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W--> 126 gacagttgaa gcaacaggaa caacaaggat gggttggtgnt gatgctgatg tgggtgatgtg      120
128 ttattcatca aatactaaat actacattac ttgttgctgc ctacttctcc tatttctctc      180
W--> 130 gccacccatt ttggaccac ganccttcca tttaaacctt ctctcgtgct attcaccaga      240
132 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcacgttta      300
134 ttaacgtaag ttttttttga ccaatcatat ctaaaatcta gtacatgcaa tagattaatg      360
136 actgttcctt cttttgatat tttcagcttc ttgaattcaa gatgggtgct ggtggaagaa      420
138 taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg      480
140 agaaaccacc attcactggt aaagatctga agaaagcaat cccacagcat tgtttcaagc      540
142 gctctatccc tegtctcttc tctaccttc tcacagatat cactttagtt tcttgcttct      600
144 actacgttgc cacaatttac ttctctcttc tctctcagcc tctctctact tacctagctt      660
146 ggccctctcta ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg      720
148 aatgtggtca ccatgcattc agtgactatc aatgggtaga tgacactggt gggtttatct      780
150 tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcacgtg cgtcaccatt      840

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152 ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900
154 aatggtatgt taaatacctc aacaaccctc ttggacgcat tctggtgtta acagttcagt 960
156 ttatcctcgg gtggcctttg tatctagcct ttaatgtatc aggtagacct tatgatggtt 1020
158 tcgcttcaca tttcttcctt catgcaccta tctttaaaga ccgagaacgc ctccagatat 1080
160 acatctcaga tgctggtatt ctagctgtct gttatggtct ttaccgttac gctgcttcac 1140
162 aaggattgac tgctatgac tgctctatg gagtaccgct tttgatagtg aactttttcc 1200
164 ttgtcttggg aactttcttg cagcacactc atccttcgtt acctcattat gattcaaccg 1260
166 agtgggaatg gattagagga gctttggtta cggtagacag agactatgga atattgaaca 1320
168 aggtgttcca taacataaca gacacacatg tggctcatca tctctttgca actataccgc 1380
170 attataacgc aatggaagct acagaggcga taaagccaat acttggtgat tactaccact 1440
172 tcgatggaac accgtggtat gtggccatgt atagggaagc aaaggagtgt ctctatgtag 1500
174 aaccggatac ggaacgtggg aagaaagggtg tctactatta caacaataag ttatgaggct 1560
176 gatagggcga gagaagtgc attatcaatc ttcatttcca tgttttaggt gtcttggtta 1620
W--> 178 agaagctatg ctttgtttca atastctcag agtccatnta gttgtgttct ggtgcatttt 1680
180 gcctagttat gtggtgtcgg aagttagtgt tcaaactgct tcctgctgtg ctgcccagtg 1740
W--> 182 aagaacaagt ttacgtgttt aaaatactcg gaacgaattg accacaanat atccaaaacc 1800
184 ggctatccga attccatata cgaaaaccgg atatccaaat ttccagagta cttag 1855

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187 <210> SEQ ID NO: 4

188 <211> LENGTH: 384

189 <212> TYPE: PRT

190 <213> ORGANISM: Lesquerella fendleri

192 <400> SEQUENCE: 4

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194 Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
195 1 5 10 15
198 Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
199 20 25 30
202 Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
203 35 40 45
206 Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
207 50 55 60
210 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
211 65 70 75 80
214 Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
215 85 90 95
218 Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
219 100 105 110
222 Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
223 115 120 125
226 Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
227 130 135 140
230 His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
231 145 150 155 160
234 Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
235 165 170 175
238 Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
239 180 185 190
242 Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
243 195 200 205
246 Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu

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247      210      215      220
250 Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
251 225      230      235      240
254 Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
255      245      250      255
258 Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
259      260      265      270
262 Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
263      275      280      285
266 Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
267      290      295      300
270 Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
271 305      310      315      320
274 Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
275      325      330      335
278 Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
279      340      345      350
282 Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
283      355      360      365
286 Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
287      370      375      380
290 <210> SEQ ID NO: 5
291 <211> LENGTH: 387
292 <212> TYPE: PRT
293 <213> ORGANISM: Ricinus communis
295 <400> SEQUENCE: 5
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298 1      5      10      15
301 Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
302      20      25      30
305 Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
306      35      40      45
309 Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
310      50      55      60
313 Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
314 65      70      75      80
317 Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
318      85      90      95
321 Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
322      100      105      110
325 His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
326      115      120      125
329 Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
330      130      135      140
333 His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
334 145      150      155      160
337 Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
338      165      170      175
341 Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu

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342          180          185          190
345 Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
346          195          200          205
349 Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
350          210          215          220
353 Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
354 225          230          235          240
357 Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
358          245          250          255
361 Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
362          260          265          270
365 Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
366          275          280          285
369 Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
370          290          295          300
373 Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
374 305          310          315          320
377 Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
378          325          330          335
381 Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
382          340          345          350
385 Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
386          355          360          365
389 Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
390          370          375          380
393 Asn Lys Tyr
394 385
397 <210> SEQ ID NO: 6
398 <211> LENGTH: 383
399 <212> TYPE: PRT
400 <213> ORGANISM: Arabidopsis thaliana
402 <400> SEQUENCE: 6
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409          20          25          30
412 Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
413          35          40          45
416 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
417          50          55          60
420 Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
421 65          70          75          80
424 Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
425          85          90          95
428 Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
429          100          105          110
432 Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
433          115          120          125
436 Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His

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RAW SEQUENCE LISTING ERROR SUMMARY

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; N Pos. 88
Seq#:3; N Pos. 46, 99, 203, 1658, 1788
Seq#:7; Xaa Pos. 384
Seq#:10; Xaa Pos. 372
Seq#:14; N Pos. 6, 12, 15
Seq#:15; N Pos. 7, 10, 16



Creation date: 07-30-2004
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Team: 1600PrintWorkingFolder
Dossier: 10680554

Legal Date: 07-22-2004

No.	Doccode	Number of pages
1	CRFE	6

Total number of pages: 6

Remarks:

Order of re-scan issued on